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Bioinformatics analysis reveals a possible risk biomarker for developing gastric cancer

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Gastric cancer (GC) is an aggressive and heterogeneous disease with poor survival. The most common type of GC is adenocarcinoma, which can be divided into two subtypes: intestinal and diffuse, according to the Laurén classification. Both intestinal and diffuse-types GC are associated with Helicobacter pylori (H. pylori) infection. However, in intestinal-type GC this infection usually progresses to invasive carcinoma through the appearance of pre-neoplastic lesions: atrophic gastritis and intestinal metaplasia. Intestinal metaplasia (IM) is histologically classified into two subtypes: the complete (CIM) and the incomplete (IIM) lesions and both subtypes of IM can progress to GC, thus the investigation of deregulated genes and molecular process responsible for this transformation is relevant. Previously, the TULP3 transcription factor was identified as a possible prognostic biomarker in pancreatic ductal adenocarcinoma. Considering that pancreatic and gastric tissues have the same embryonic origin, we investigated the profile of TULP3 expression in gastric tissues hypothesizing that it may have a role in gastric diseases. We comparatively analyzed TULP3 expression in different gastric tissues through the in gene expression data publicly available using bioinformatics tools, and we verified TULP3 gene expression association with patient survival in GC. We found a significant statistical difference between groups in GSE2669 study (p-value=3.435e-05), in which non-tumoral gastric lesions have similar TULP3 gene expression (ChG median=0.152 and IM median=0.158). We also observed in GSE78523 study higher TULP3 levels in incomplete IM subtype that progressed to GC (IIM-GC) in comparison to complete IM that progressed and did not progressed to GC (CIM-GC and CIM-nonGC) with a significant statistical difference (p-value=2.488e-03). The IM lesion is characterized by the replacement of gastric mucosa normal epithelium to an intestinal one and the incomplete (IIM) subtype is more likely to progress to GC than the complete (CIM). Thus, the TULP3 gene expression in the progression from intestinal metaplasia to gastric carcinoma indicates a possible role as risk biomarker for developing gastric cancer. Palavras-chaves: gastric cancer, intestinal metaplasia, TULP3